

Sequence 52, Application US/0917340
Patent No. US200200369A1
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McNulty, Jonathan P.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
PRIOR FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 66/221,632
PRIOR FILING DATE: 2000-07-29
PRIOR APPLICATION NUMBER: 66/249,632
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 66/290,912
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 52
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-52

Query Match 100.0%; Score 250; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 1e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINTLQKYYVRGRCVAVSLCPKEQIGKSTRGKCKRRK 45
DB 23 GINTLQKYYVRGRCVAVSLCPKEQIGKSTRGKCKRRK 67

RESULT 3
US-09-917-340-72
Sequence 72, Application US/0917340
Patent No. US200200369A1
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McNulty, Jonathan P.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
PRIOR FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 66/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 66/249,632
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 66/290,912
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 72
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-72

Query Match 100.0%; Score 250; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 1e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINTLQKYYVRGRCVAVSLCPKEQIGKSTRGKCKRRK 45
DB 23 GINTLQKYYVRGRCVAVSLCPKEQIGKSTRGKCKRRK 67

RESULT 4
US-09-872-852-2
Sequence 2, Application US/09872852
Patent No. US2002015602A1
GENERAL INFORMATION:

APPLICANT: MCCRAY JR, PAUL B.
APPLICANT: TACK, BRIAN
APPLICANT: STA, HENNING
APPLICANT: MCGILL, BRENN
TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC
TITLE OF INVENTION: BETA-DEFENSIN ANTIMICROBIAL PEPTIDE
FILE REFERENCE: TOMA-031US
CURRENT APPLICATION NUMBER: US/09/872,852
CURRENT FILING DATE: 2001-04-01
PRIOR APPLICATION NUMBER: 60/238,792
PRIOR FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 2
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-872-852-2

Query Match 100.0%; Score 250; DB 10; Length 67;
Best Local Similarity 100.0%; Pred. No. 1e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINTLQKYYVRGRCVAVSLCPKEQIGKSTRGKCKRRK 45
DB 23 GINTLQKYYVRGRCVAVSLCPKEQIGKSTRGKCKRRK 67

RESULT 5
US-10-091-165B-10
Sequence 10, Application US/091165B
Patent No. US2002015602A1
GENERAL INFORMATION:
APPLICANT: Adelman, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baicker, David
APPLICANT: Seigel-Quin, Stephanie
APPLICANT: Sheppard, Paul C.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-4401
CURRENT APPLICATION NUMBER: US/10/091,165B
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: US/07/436,339
PRIOR FILING DATE: 2000-09-10
PRIOR APPLICATION NUMBER: US/08/144,097
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US/07/50,756
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: US/07/364,254
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US/07/058,335
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 1
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-10-091-165B-10

Query Match 100.0%; Score 250; DB 12; Length 67;
Best Local Similarity 100.0%; Pred. No. 1e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINTLQKYYVRGRCVAVSLCPKEQIGKSTRGKCKRRK 45
DB 23 GINTLQKYYVRGRCVAVSLCPKEQIGKSTRGKCKRRK 67

RESULT 6

Query Match: 100.0%; S00x: 250; D0: 12; Length: 67;

NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 65
TYPE: PRT
ORGANISM: Homo sapiens
US-10-C9-166B-2

Query Match
Best Local Similarity 96.04, Score 240, DB 12, Length 65,
Matches 43, Conservative 0, Mismatches 0, Indels 0, Gaps 0
QY 1 GINTLQYVYVGRGCAVLSCLPKSEQ:OKCSTRGRKCCR 43
DB 23 GINTLQYVYVGRGCAVLSCLPKSEQ:OKCSTRGRKCCR 65

RESULT 13
US-10-439-366-2
Sequence 2, Application US/1022121
Publication No. US200301562A1
GENERAL INFORMATION:
APPLICANT: Adet, David A.
APPLICANT: Holladay, James L.
APPLICANT: Belindur, Nand
APPLICANT: Beigel-Ome, Stephanie
APPLICANT: Shepard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/1022121-121
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 09/636,399
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/344,597
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/150,786
PRIOR FILING DATE: 1998-09-13
PRIOR APPLICATION NUMBER: US 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 63/058,355
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 65
TYPE: PRT
ORGANISM: Homo sapiens
US-10-439-366-2

Query Match
Best Local Similarity 96.04, Score 243, DB 12, Length 65,
Matches 43, Conservative 0, Mismatches 0, Indels 0, Gaps 0
QY 1 GINTLQYVYVGRGCAVLSCLPKSEQ:OKCSTRGRKCCR 43
DB 23 GINTLQYVYVGRGCAVLSCLPKSEQ:OKCSTRGRKCCR 65

RESULT 11
US-10-439-366-2
Sequence 2, Application US/0459366
Publication No. US2003016692A1
GENERAL INFORMATION:
APPLICANT: Adet, David A.
APPLICANT: Holladay, James L.
APPLICANT: Beigel-Ome, Stephanie
APPLICANT: Shepard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/10409366
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US/09/636,399A

PRIOR FILING DATE: 2002-08-10
PRIOR APPLICATION NUMBER: 62/555,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 66/764,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/50,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,359
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 2
LENGTH: 65
TYPE: PRT
ORGANISM: Homo sapiens
US-10-439-366-2

Query Match
Best Local Similarity 96.04, Score 240, DB 12, Length 65,
Matches 43, Conservative 0, Mismatches 0, Indels 0, Gaps 0
QY 1 GINTLQYVYVGRGCAVLSCLPKSEQ:OKCSTRGRKCCR 43
DB 23 GINTLQYVYVGRGCAVLSCLPKSEQ:OKCSTRGRKCCR 65

RESULT 12
US-10-439-362-2
Sequence 2, Application US/0409532
Publication No. US2003015693A1
GENERAL INFORMATION:
APPLICANT: Adet, David A.
APPLICANT: Holladay, James L.
APPLICANT: Beigel-Ome, Stephanie
APPLICANT: Shepard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/10409362
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US/09/636,399A
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 62/555,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-13
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 2
LENGTH: 65
TYPE: PRT
ORGANISM: Homo sapiens
US-10-439-362-2

Query Match
Best Local Similarity 96.04, Score 240, DB 12, Length 65,
Matches 43, Conservative 0, Mismatches 0, Indels 0, Gaps 0
QY 1 GINTLQYVYVGRGCAVLSCLPKSEQ:OKCSTRGRKCCR 43
DB 23 GINTLQYVYVGRGCAVLSCLPKSEQ:OKCSTRGRKCCR 65

RESULT 13
US-09-872-852-3
Sequence 3, Application US/092882
Patent No. US02015632A1
GENERAL INFORMATION:
APPLICANT: MCCRAY JR, PAUL B.

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1 APPLICANT: TUCK, BRIAN
2 APPLICANT: JIA, HONG FENG
3 APPLICANT: HOLLOWAY, DAVID A.
4 TITLE OF INVENTION: BETA-DEFENSIN-3 (HBB-3), A HIGHLY CATIONIC
5 TITLE OF INVENTION: BETA-DEFENSIN ANTI-MICROBIAL PEPTIDE
6 FILE REFERENCE: IOWA-03105
7 CURRENT APPLICATION NUMBER: US/09/872,852
8 CURRENT FILING DATE: 2001-06-01
9 PRIOR APPLICATION NUMBER: 60/208,792
10 PRIOR FILING DATE: 2003-06-01
11 NUMBER OF SEQ ID NOS: 24
12 SOFTWARE: Patent-Ver. 2.1
13 LENGTH: 41
14 TYPE: PR
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
18 OTHER INFORMATION: Peptide
19 US-09-872-852-3
20
21 Query Match 92.00; Score 210; DB 10; Length 41;
22 Best Local Similarity 91.10; Pred No 1, 9e-19;
23 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OK protein - protein search, using sw model

Run On: October 27, 2003, 14:52:02 : Search time 16 seconds
270,474 Million cell updates/sec

Title: US-09-872-852-4
Perfect score: 250
Sequence: 1 FNTVQXNYVRGNCAY.....KEEIGKCGTGRKRCRRK 45

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 203308 seqs, 96168692 residues
Total number of hits satisfying chosen parameters: 203308

Minimum 26 seq length: 6
Maximum 26 seq length: 200000000
Post-processing: Minimum Match 0
Maximum Match 100
Listing first 45 summaries

Database: PIR761
1. PIR761
2. PIR761
3. PIR761
4. PIR761

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	35.6	42	F45495	beta-defensin-6
2	75	30.0	38	B47953	beta-defensin-11
3	73	27.2	64	A56128	lingual antimicrobial
4	71	25.4	42	C45435	beta-defensin-3
5	71	25.4	64	A47438	airway epithelial
6	69.5	27.8	45	A73309	myotoxin - elastin
7	69.5	27.8	42	M12301	macrophage antibio
8	69.5	27.8	42	M12301	macrophage antibio
9	68	27.6	40	F45496	beta-defensin-9
10	68	27.2	42	D47753	beta-defensin-13
11	67.5	27.0	65	C15947	crotamine 3 precursor
12	67.5	27.0	65	A35947	crotamine 1 precursor
13	66.5	26.6	43	C15947	toxic peptide C
14	65.5	26.2	42	C15947	crotamine 4 precursor
15	65.5	26.2	51	C15947	crotamine 3 precursor
16	65.5	26.2	35	W18B92	defensin CS-4 precursor
17	63.5	23.4	45	M43341	myotoxin a precursor
18	63.5	23.4	45	M43341	myotoxin a precursor
19	62.5	24.4	42	S18539	defensin alpha-4
20	61	24.4	67	I45957	disintegrin-like
21	61.5	24.2	40	C15940	myotoxin a - pra
22	61	24.0	32	C15940	defensin alpha-5
23	60	24.0	32	E59076	defensin alpha-7
24	60	24.0	31	D59076	defensin alpha-4
25	60	24.0	31	E59076	defensin alpha-6
26	59	23.6	45	F45495	beta-defensin-13
27	59	23.6	45	F45495	myotoxin - midline
28	59.5	23.4	43	A20309	myotoxin - western
29	56.5	23.4	45	S12959	myotoxin - western

High sulfur proteol
probable finger pr
corticosterone bet
protamine - mouse
protamine 1 - rat
myosin-11 - mid
hypocretin, pice
hypocretin, pice
genom polypeptide
Xcr-2 protein
defensin alpha-5 p
epidermal growth f
epidermal growth f
epidermal growth f
epidermal growth f
galinacin - chick

ALIGNMENTS

RESULT 1

F45495
beta-defensin-6 bovine
C:Accession: F45495
C:Date: 14-Feb-1994 #sequence-revision 22-Apr-1995 #ext-change 25-Oct-1996
C:Accession: F45495
P:Seisles, N.E.; Tang, Y.Q.; Norris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.J.
C: Biol. Chem. 268, 6641-6648, 1993
A:Title: Purification, primary structures, and antibacterial activities of beta-defe
A:Reference number: A45495; MUID 9323264; PMID:8454635
A:Accession: F45495
A:Molecule type: Protein
A:Note: Sequence modified after extraction from NCBI backbone
C:Keywords: antibacterial; disulfide bond; pyroglutamic acid
P:142/2/Product: beta-defensin-6 status experimental <NA>
P:1/Modified site: pyroglutamic acid (Gln) status experimental
P:9318,16-31,21-39/2/Disulfide bonds: status Predicted

Query Match 35.64; Score 69; DR 2; Length 42;

Best local similarity 48.51; Pred. MC 3.0042;
Matches 16; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 11 CAVSAGKAVLSCEVKEEDKGRKRCRR 43
DQ 9 LAYVQCVPEICRGRTRCTTCEFPVACRR 41

RESULT 2

B47953
beta-defensin-11 bovine
C:Accession: B47953
C:Date: 14-Feb-1994 #sequence-revision 18-Nov-1994 #ext-change 16-Dec-1998
P:Seisles, N.E.; Tang, Y.Q.; Norris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.J.
C: Biol. Chem. 268, 6641-6648, 1993
A:Title: Purification, primary structures, and antibacterial activities of beta-defe
A:Reference number: A45495; MUID 9323264; PMID:8454635
A:Accession: B47953
A:Molecule type: Protein
A:Note: Sequence modified after extraction from NCBI backbone
C:Keywords: antibacterial; disulfide bond
P:142/2/Product: beta-defensin-11 status experimental <NA>
P:14,12-27,19/2/Disulfide bonds: status Predicted

Query Match 30.01; Score 62; DR 2; Length 42;

Best local similarity 36.91; Pred. MC 3.0042;
Matches 15; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

QY 11 CTVRGRCNVLSLPKNSVIGKSTGRKCR 42
Do 5 CERNQGVPCVPCPQPNVIGTCFGRVKCR 35

RESULT 3
A56128
Lingual antimicrobial peptide precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Nov-1999
C:Accession: A56128, E56128, B56128
R:Schwartz, M.J., 1995
A:Title: Epithelial antibodies induced at sites of inflammation
A:Reference number: A56128; M010:05152714; PMID:188645
A:Accession: A56128
A:Molecule type: mRNA
A:Residues: 1-64 <S>
A:Cross-references: SB:574275; NID:9694208; FIDN:AA813727.1; PID:9594209
A:Accession: B56128
A:Molecule type: Protein
A:Residues: 23-64 <S>
C:Keywords: antibacterial; antifungal
F:23-64/Product: lingual antimicrobial peptide status predicted <SIG>
F:23-64/Product: lingual antimicrobial peptide status experimental <MAT>

Query Match 29.21; Score 73; DB 2; Length 64;
Best Local Similarity 44.11; Pred. No. 0.052;
Matches 15; Conservative 1; Mismatches 15; Indels 0; Gaps 0;

QY 11 CTVRGRCNVLSLPKNSVIGKSTGRKCR 44
DB 31 CERNQGVPCVPCPQPNVIGTCFGRVKCR 64

RESULT 4
C45495
beta-defensin-3 - bovine
N:Alternate names: peptide BN30-3
X:Contains: beta-defensin-2
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 23-Oct-1996
C:Accession: C45495; B45495
R:Salicrú, M.E.; Tang, Y.Q.; Morris, W.D.; McGuire, P.A.; Novotny, M.J.; Strich, K.; Heng
J.; Biol. Chem. 269, 6641-6645, 1993
A:Title: Purification, primary structure, and antibacterial activities of beta-defensin
A:Accession: C45495; B45495; NID:9202094; PMID:8454635
A:Molecule type: Protein
A:Residues: 1-42 <SEL>
A>Note: sequence modified after extraction from NCBI backbone
A:Molecule type: Protein
A:Residues: 3-42 <S>
A:Note: sequence extracted from NCBI backbone (NCBI:127952)
C:Keywords: antibacterial; disulfide bond; pyroglutamic acid
F:1-42/Product: beta-defensin-3 status experimental <MAT>
F:1-42/Product: beta-defensin-3 status predicted <SIG>
F:1-42/Product: beta-defensin-3 status experimental <MAT>
F:19-36-16-31-21-35/Disulfide bonds: #status predicted

Query Match 28.41; Score 71; DB 2; Length 42;
Best Local Similarity 40.63; Pred. No. 0.065;
Matches 13; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

QY 11 CTVRGRCNVLSLPKNSVIGKSTGRKCR 42
DB 9 CERNQGVPCVPCPQPNVIGTCFGRVKCR 40

RESULT 5
A47414
airway epithelial antimicrobial peptide precursor - bovine

N:Alternate names: antimicrobial peptide, tracheal
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: A47418; A19397
S:Diamond, G.; Conns, D.E.; Bevins, C.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 4596-4600, 1993
A:Title: Airway epithelial cells are the site of expression of a mammalian antimicro
A:Reference number: A47418; M010:93281625; PMID:856105
A:Accession: A47418
A>Status: preliminary
A:Molecule type: cDNA
A:Cross-references: GR:133771; NID:9289195; PIDN:AA472363.1; PID:9289195
R:Diamond, G.; Zaslavsky, M.; Eck, H.; Brasseur, M.; Maloy, W.L.; Bevins, C.L.
Proc. Natl. Acad. Sci. U.S.A. 89, 1952-1956, 1992
A:Title: Tracheal antimicrobial peptide, a cysteine-rich peptide from mammalian tra
A:Reference number: A39397; M010:92119450; PMID:1023943
A:Accession: A39397
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-64 <S>
C:Cross-references: SB:561673; NID:9226433; FIDN:AA81757.1; PID:9161742
A:Accession: A39397
F:1-64/Product: airway epithelial antimicrobial peptide TAP status predicted <MAT>

Query Match 18.41; Score 71; DB 2; Length 64;
Best Local Similarity 41.21; Pred. No. 0.031;
Matches 14; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

QY 11 CTVRGRCNVLSLPKNSVIGKSTGRKCR 44
DB 31 CERNQGVPCVPCPQPNVIGTCFGRVKCR 64

RESULT 6
A37903
myotxin - eastern diamondback rattlesnake
C:Species: Crotalus adamanteus leisteri diamondback rattlesnake
C:Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 11-Nov-1994
C:Accession: A37903
R:Sarejani, Y.; Aoki, Y.; Webb, D.
Toxicol. 29, 461-469, 1991
A:Title: Anti-endothelial cell activity of a myotoxin from venom of the eastern diamondback r
A:Accession: A37903
A:Cross-references: A37903
A:Molecule type: Protein
A:Residues: 1-45 <SAV>
A:Superfamily: crotoxin
C:Keywords: myotoxin

Query Match 27.81; Score 69.5; DB 2; Length 45;
Best Local Similarity 38.91; Pred. No. 0.1;
Matches 14; Conservative 4; Mismatches 15; Indels 3; Gaps 2;

QY 11 CTVRGRCNVLSLPKNSVIGKSTGRKCR 43
DB 4 CERNQGVPCVPCPQPNVIGTCFGRVKCR 39

RESULT 7
A47414
macrophage antibiotic peptide MCP-1 - rabbit
N:Alternate names: antiadrenocorticotropic, corticostatic peptide CS-3; defensin
C:Species: cryptotrigus chalcidus (domestic rabbit)
C:Date: 28-Aug-1993 #sequence_revision 08-Nov-1996 #text_change 18-Jun-1999
R:Garcia, J.N.; Vilella, E.V.; Tuncio, A.; Talmadge, K.; Fuller, F.
J. Immunol. 153, 1358-1365, 1994
A:Title: The structure of the rabbit macrophage defensin genes and their organ-spec
A:Reference number: A45911; M010:89309825; PMID:12745593

```

A.Accession: A45495
A.Status: preliminary
A.Molecule type: RNA
A.Molecule type: RNA
A.Residues: 1-95 <GAG>
A.Cross-references: GB:28072; NCID:Q165473; PICB:AA31362.1; PID:G15474
R.SeqListed: M.E.; Brown, D.M.; DeGange, R.M.; Lehter, R.I.
J.Biol. Chem. 258: 14485-14489, 1983
A.Title: Primary structures of MCP-1 and MCP-2, natural peptide antibiotics of rabbit
A.Reference number: A01647; MIMD:840619C1; PMID:664347
A.Accession: A01647
A.Molecule type: protein
A.Residues: 1-95 <GAG>
R.SeqListed: M.E.; Brown, D.M.; DeGange, R.M.; Lehter, R.I.
J.Biol. Chem. 258: 14485-14489, 1983
A.Title: Primary structures of six antimicrobial peptides of rabbit peritoneal neutrophils
A.Reference number: A22569; MIMD:8512561; PMID:1398276
A.Accession: A22569
A.Molecule type: protein
A.Residues: 63-95 <SE2>
A.Experimental source: peritoneal neutrophils
R.Author: Q.; Solomon, S.J.; 1433, 1992
A.Title: Isolation and mode of action of rabbit corticosteroid (antiadrenocorticotropin)
A.Reference number: A49195; MIMD:92164516; PMID:1311240
A.Accession: A49195
A.Status: preliminary
A.Molecule type: protein
A.Residues: 63-95 <HD>
A.Note: sequence extracted from NCBI backbone (NCBI:85978)
C.Comment: This peptide is active against some fungi and gram-positive bacteria in vitro
C.Superfamily: mammalian defensin
P:38-99,67-87,72-92/Disulfide bonds: #status predicted

Query Match 27.61; Score 69.5; DB 1; Length 95;
Best Local Similarity 48.31; Pred. No. 0.13;
Matches 14; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

QY 18 CAVSLCPKEEDIKCKSTGR--KCCR 43
Db 67 CFAALCPENRAGTGRKGRHFCR 95

RESULT 4
G45495
A.Alternate names: peptide BNB0-7
C.Species: Bos primigenius taurus (cattle)
C.Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #ext_change 28-Oct-1994
A.Accession: G45495
R.SeqListed: M.E.; Brown, D.M.; DeGange, R.M.; Lehter, R.I.
J.Biol. Chem. 258: 14485-14489, 1983
A.Title: Purification, primary structures, and antibacterial activities of beta-defensin
A.Reference number: A45495; MIMD:9303264; PMID:8454635
A.Accession: G45495
A.Molecule type: protein
A.Residues: 1-40 <SE2>
A.Note: sequence modified after extraction from NCBI backbone
C.Keywords: antibacterial; disulfide bond; pyroglutamic acid
P:1-40/Product: beta-defensin-3 #status experimental <MA>
P:38-116,71-93/Disulfide bonds: #status experimental
P:9-38,16-71,22-93/Disulfide bonds: #status predicted

Query Match 27.61; Score 69; DB 2; Length 40;
Best Local Similarity 40.61; Pred. No. 0.11;
Matches 13; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

QY 11 CAVRGPCAVLSLPKEEDIKCKSTGRKCCR 42
Db 9 CAVRGPCAVLSLPKEEDIKCKSTGRKCCR 40

RESULT 3
G45495
A.Alternate names: peptide BNB0-3
C.Species: Bos primigenius taurus (cattle)
C.Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #ext_change 28-Apr-1995
A.Accession: G45495
R.SeqListed: M.E.; Brown, D.M.; DeGange, R.M.; Lehter, R.I.
J.Biol. Chem. 258: 14485-14489, 1983
A.Title: Purification, primary structures, and antibacterial activities of beta-defensin
A.Reference number: A45495; MIMD:9303264; PMID:8454635
A.Accession: G45495
A.Molecule type: protein
A.Residues: 1-40 <SE2>
A.Note: sequence modified after extraction from NCBI backbone
C.Keywords: antibacterial; disulfide bond; pyroglutamic acid
P:1-40/Product: beta-defensin-3 #status experimental <MA>
P:38-116,71-93/Disulfide bonds: #status experimental
P:9-38,16-71,22-93/Disulfide bonds: #status predicted

Query Match 27.61; Score 69; DB 2; Length 40;
Best Local Similarity 40.61; Pred. No. 0.11;
Matches 13; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

QY 11 CAVRGPCAVLSLPKEEDIKCKSTGRKCCR 42
Db 9 CAVRGPCAVLSLPKEEDIKCKSTGRKCCR 40

RESULT 11
G3547
A.Alternate names: topical, rat defensin
C.Species: Rattus norvegicus (brown rat)
C.Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #ext_change 24-Jun-1993

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A45495
A.Alternate names: peptide BNB0-3
C.Species: Bos primigenius taurus (cattle)
C.Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #ext_change 28-Apr-1995
R.SeqListed: M.E.; Brown, D.M.; DeGange, R.M.; Lehter, R.I.
J.Biol. Chem. 258: 14485-14489, 1983
A.Title: Purification, primary structures, and antibacterial activities of beta-defensin
A.Reference number: A45495; MIMD:9303264; PMID:8454635
A.Accession: A45495
A.Molecule type: protein
A.Residues: 1-40 <SE2>
A.Note: sequence modified after extraction from NCBI backbone
C.Keywords: antibacterial; disulfide bond; pyroglutamic acid
P:1-40/Product: beta-defensin-3 #status experimental <MA>
P:38-116,71-93/Disulfide bonds: #status experimental
P:9-38,16-71,22-93/Disulfide bonds: #status predicted

Query Match 27.61; Score 69; DB 2; Length 40;
Best Local Similarity 40.61; Pred. No. 0.11;
Matches 13; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

QY 11 CAVRGPCAVLSLPKEEDIKCKSTGRKCCR 42
Db 9 CAVRGPCAVLSLPKEEDIKCKSTGRKCCR 40

RESULT 10
D4755
A.Alternate names: peptide BNB0-13
C.Species: Beta defensin-12
C.Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #ext_change 22-Apr-1995
A.Accession: D4755
R.SeqListed: M.E.; Brown, D.M.; DeGange, R.M.; Lehter, R.I.
J.Biol. Chem. 258: 14485-14489, 1983
A.Title: Purification, primary structures, and antibacterial activities of beta-defensin
A.Reference number: A45495; MIMD:9303264; PMID:8454635
A.Accession: D4755
A.Molecule type: protein
A.Residues: 1-42 <SE1>
A.Note: sequence extracted from NCBI backbone (NCBI:127563)
A.Accession: D4755
R.SeqListed: M.E.; Brown, D.M.; DeGange, R.M.; Lehter, R.I.
J.Biol. Chem. 258: 14485-14489, 1983
A.Title: Purification, primary structures, and antibacterial activities of beta-defensin
A.Reference number: A45495; MIMD:9303264; PMID:8454635
A.Accession: D4755
A.Molecule type: protein
A.Residues: 1-42 <SE1>
A.Note: sequence extracted from NCBI backbone
C.Keywords: antibacterial; disulfide bond
P:1-42/Product: beta-defensin-13 #status experimental <MA>
P:5-42/Product: beta-defensin-12 #status experimental <MA>
P:9-39,16-31,21-35/Disulfide bonds: #status experimental

Query Match 27.24; Score 65; DB 2; Length 42;
Best Local Similarity 43.24; Pred. No. 0.16;
Matches 14; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

QY 11 CAVRGPCAVLSLPKEEDIKCKSTGRKCCR 42
Db 9 CAVRGPCAVLSLPKEEDIKCKSTGRKCCR 40

RESULT 11
G3547
A.Alternate names: topical, rat defensin
C.Species: Rattus norvegicus (brown rat)
C.Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #ext_change 24-Jun-1993

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C:Accession: C35947
R:Protein: Schmitt, J.J.
Toxinon 28, 576-585, 1990.
A:Title: Cloning and nucleotide sequences of crocaine genes.
A:Reference number: A35947; MUID:90357261; PMID:2389256
A:Accession: C35947
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-45 <SM1>
C:Superfamily: crocaine

Query Match 27.04; Score 67.5; DB 1; Length 65;
Best Local Similarity 37.84; Pred. No. 0.25;
Matches 14; Conservative 5; Mismatches 13; Indels 5; Gaps 3;

QY 11 CRYVGRCAVLS--CLKEKEDQIK--CSTRKRCRR 43
DB 26 CHIKGRCFFPKXKICIFPSDFGMDCKR--KCKCK 61

RESULT 12
A:Species: 1 precursor - tropical rattlesnake
C:Species: Crocatus durissus terrificus (tropical rattlesnake, cascade).
C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 24-Jun-1993
C:Accession: A15947
R:Smith, L.A.; Schmidt, J.J.
Toxinon 28, 576-585, 1990.
A:Title: Cloning and nucleotide sequences of crocaine genes.
A:Reference number: A15947; MUID:90357261; PMID:2389256
A:Accession: A15947
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-45 <SM1>
C:Superfamily: crocaine

Query Match 27.04; Score 67.5; DB 1; Length 65;
Best Local Similarity 37.84; Pred. No. 0.25;
Matches 14; Conservative 5; Mismatches 13; Indels 5; Gaps 3;

QY 11 CRYVGRCAVLS--CLKEKEDQIK--CSTRKRCRR 43
DB 26 CHIKGRCFFPKXKICIFPSDFGMDCKR--KCKCK 61

RESULT 13
C:Species: 1 precursor - southern Pacific rattlesnake
C:Species: Crocatus viridis helleri (southern Pacific rattlesnake)
C:Date: 31-May-1979 #sequence_revision 08-Oct-198; #text_change 23-Aug-1996
C:Accession: A01737
R:Maeda, N.; Taniya, N.; Pattabhiraman, T.R.; Russell, F.F.
Toxinon 16, 431-441, 1978
A:Title: Some chemical properties of the venom of the rattlesnake, Crocatus viridis helleri
A:Accession: A01737
A:Status: preliminary; not compared with conceptual translation
A:Residues: 1-41 <SM1>
A:Keywords: avicoxin; venom
C:Superfamily: crocaine
P:4-36,11-30,18-37/Disulfide bonds: #status predicted

Query Match 26.64; Score 66.5; DB 1; Length 43;
Best Local Similarity 36.14; Pred. No. 0.23;
Matches 13; Conservative 5; Mismatches 15; Indels 3; Gaps 2;

QY 11 CRYVGRCAVLS--CLKEKEDQIK--CSTRKRCRR 43
DB 4 CHIKGRCFFPKXKICIFPSDFGMDCKR--KCKCK 39

RESULT 14
C:Species: 1 precursor - tropical rattlesnake
C:Species: Crocatus durissus terrificus (tropical rattlesnake, cascade)
C:Date: 22-Jun-1991 #sequence_revision 22-Jun-199; #text_change 23-Aug-1996
C:Accession: A01735
R:Lauro, C.J.
Heppe-Seyler's 2. Physiol. Chem 356, 213-215, 1975
A:Title: The primary structure of crocaine, a basic toxin isolated from the venom of
A:Reference number: A01735; MUID:76023761; PMID:1176386
A:Accession: A01735
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: protein
A:Residues: 1-42 <SM1>
A:Keywords: avicoxin; venom
C:Superfamily: crocaine
P:4-16,11-30,18-37/Disulfide bonds: #status predicted

Query Match 26.24; Score 65.5; DB 1; Length 42;
Best Local Similarity 35.94; Pred. No. 0.3;
Matches 14; Conservative 3; Mismatches 16; Indels 3; Gaps 2;

QY 11 CRYVGRCAVLS--CLKEKEDQIK--CSTRKRCRR 43
DB 4 CHIKGRCFFPKXKICIFPSDFGMDCKR--KCKCK 39

RESULT 15
C:Species: 4 precursor - tropical rattlesnake (fragment)
C:Species: Crocatus durissus terrificus (tropical rattlesnake, cascade)
C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 24-Jun-1993
C:Accession: C15947
R:Smith, L.A.; Schmidt, J.J.
Toxinon 28, 576-585, 1990
A:Title: Cloning and nucleotide sequences of crocaine genes.
A:Reference number: A15947; MUID:90357261; PMID:2389256
A:Accession: C15947
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-45 <SM1>
C:Superfamily: crocaine

Query Match 24.24; Score 65.5; DB 1; Length 51;
Best Local Similarity 35.14; Pred. No. 0.35;
Matches 13; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY 11 CRYVGRCAVLS--CLKEKEDQIK--CSTRKRCRR 44
DB 12 CHIKGRCFFPKXKICIFPSDFGMDCKR--KCKCK 48

Search completed: October 27, 2003, 14:53:23
CPU time: 1.8 sec

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P. AERUGINOSA AND E. COLI AND THE YEAST CALBICUMS. KILLS MULTIRESTANT S. AUREUS AND VANCOMYCIN-RESISTANT E. FAECIUM. NO SIGNIFICANT HEMOLYTIC ACTIVITY WAS OBSERVED.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -2- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SKIN AND TONGUES, AND TO A LESSER EXTENT IN TRACHEA, UTERUS, KIDNEY, THYMUS, ADENOID, PHARYNX AND TONGUE. LOW EXPRESSION IN SALIVARY GLAND, BOVINE VAGINA, COLON.

CC -3- FUNCTION: LOW EXPRESSION IN SALIVARY GLAND, BOVINE VAGINA, COLON.

CC -4- FUNCTION: BY INFECTING BOVINE INTERFERON- γ DEFICIENT.

CC -5- MASS SPECTROMETRY: M44514.50; YETHAQLE; ESTIMATED; RANGE:21.6V.

CC -6- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.

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CC EMBL: A731767.1; GAC31797.1; .

CC EMBL: AF296370.1; AG32237.1; .

CC EMBL: AF214245.1; AAF71653.1; .

CC EMBL: AB017972.1; BAB43572.1; .

CC EMBL: AF311470.1; AAG22010.1; .

CC PDB: 1KJ6, 2C-MAR-02.

CC Genes: HNC15367; DEFB133.

CC MIM: 606611; .

CC GO: CC:0005567; Extracellular; NAS.

CC GO: CC:0002247; F-Gram-positive antibacterial peptide activity; TAS.

CC GO: CC:0005950; Gram-negative bacterial polypeptide in; TAS.

CC GO: CC:0005950; Gram-negative bacterial polypeptide in; TAS.

CC PDB: PFC0711; Defense; Smell; Beta.

CC Antibiotic; Signal; 30-Structure.

CC SIGNAL 23 67

CC CHAIN 23 67 BETA-DEFENSIN 1.

CC DISULFID 33 62 BY SIMILARITY.

CC DISULFID 40 55 BY SIMILARITY.

CC DISULFID 45 53 BY SIMILARITY.

CC SEQUENCE 67 AA; 7697 MW; 54266DE1C9574865 CRC64.

Query Match 100.0% Score 250.0 DB 1; Length 67;

Best Local Similarity 100.0% Pred No. 1; Gaps 0;

Matches 45; Conservative 0; Mismatches 0; Indels 0;

CC 1 GINTLQYVYVQRCAVLSCLPKEQIKSTGRKCKRKK 45

CC 23 GINTLQYVYVQRCAVLSCLPKEQIKSTGRKCKRKK 67

RESULT 2

9006 BOVIN

AD BOV12 BOVIN STANDARD. PRT: 42 AA.

DT 01-NOV-1995 (Ref. 32, Created).

DT 01-FEB-1996 (Ref. 33, Last sequence update).

DT 28-FEB-2003 (Ref. 41, Last annotation update).

DE Beta-defensin 6 (BN30-6) (BN30-6).

GN DEFB6.

OS Bos taurus (Bovine).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bovinae; Bos.

CC NCBI_TaxID=9913.

CC SEQUENCE

CC MEDLINE:9101041, PubMed:9154255.

CC Seitz M.E., Tang Y.-Q., Morris W.L., McGuire F.A., Novotny V.J., Smith W., Henschen A.H., Cullor J.S., Purification, primary structures, and antibacterial activities of beta-defensins, a new family of antimicrobial peptides from bovine neutrophils.

CC EMBL: AF46773.1; LBNB.

CC InterPro: IPR013555; Defense; Beta.

CC InterPro: PRO0493; Defense; Mammal.

CC SMART: SM00448; DEFEN; Beta; .

CC SMART: SM00448; DEFEN; Beta; .

CC ANTI-BIOTIC: PYRROLIDONE CARBOXYLIC ACID.

CC YCD RES 9 33 BY SIMILARITY.

CC DISULFID 16 31 BY SIMILARITY.

CC DISULFID 21 30 BY SIMILARITY.

CC SEQUENCE 42 AA; 4835 MW; C9AEE5ECCAE907 CRC64.

Query Match 48.6% Score 99; DB 1; Length 42;

Best Local Similarity 48.6% Pred No. 4; Gaps 0;

Matches 15; Conservative 1; Mismatches 14; Indels 0;

CC 1 CPYSGGVTF:RCPGRTQ:GICGFRPVKCR 41

CC 9 CPYSGGVTF:RCPGRTQ:GICGFRPVKCR 41

RESULT 3

BDOT_BOVIN

AD BOV12 BOVIN STANDARD. PRT: 53 AA.

CC CLARIS 18 38 Created:

CC 15-JUN-1999 (Ref. 38, Last sequence update).

CC 15-JUN-1999 (Ref. 38, Last sequence update).

CC Beta-defensin C7 precursor (BD07C7) (fragment).

CC Bos taurus (Bovine).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bovinae; Bos.

CC NCBI_TaxID=9913.

CC SEQUENCE FROM N.A.

CC 1553Small intestine.

CC Vector: pET28a(+); NumSeq:949394.

CC Expression: 100% in E. coli BL21(DE3).

CC Expression: 100% in E. coli BL21(DE3).

CC Kines M.; Baeys S.; Baeys C.L.;

CC "Enteric beta-defensin: molecular cloning and characterization of a gene with inducible intestinal epithelial cell expression associated with Cryptosporidium parvum infection."

CC Infect. Immun. 66:1045-1051:1998.

CC -1- FUNCTION: HAS PACTERICIDAL ACTIVITY.

CC -2- SUBCELLULAR LOCATION: Secreted.

CC -3- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.

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CC EMBL: AF06358; AAC4882.1; .

CC EMBL: AF67701.1; LBNB.

CC InterPro: IPR013555; Defense; Beta.

CC InterPro: PRO0493; Defense; Mammal.

CC SMART: PFC0711; Defense; Beta; .

CC SMART: SM00448; DEFEN; Beta; .

CC ANTI-BIOTIC: Signal.

CC YCD RES 4 1

CC DISULFID 4 1

CC SEQUENCE 4 1

CC POTENTIAL.

```

PT CHAIN 16 53 BETA-DEFENSIN CT.
PT DISULFID 20 43 BY SIMILARITY
PT DISULFID 27 42 BY SIMILARITY
PT DISULFID 32 50 BY SIMILARITY
SQ SEQUENCE 53 AA: 5650 DEF1A0483FA CRC64.
Query Match 32.0% Score 86; DB 1; Length 53;
Best Local Similarity 46.9% Pred. No. 0 COL1;
Matches 15: Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 11 EVNGRCVAVSCLPKBEQIGKSTPRKCR 42
DE 20 TARKNGDILLRCQWQWQIQTFQRPVKCR 51

RESULT 4
ID_EAP_BOVIN STANDARD PRT: 64 AA.
AC G52775.
DT 31-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-2001 (Rel. 42, Last annotation update)
DE Beta-defensin 1; Precursor (SD-1) (Defensin, beta 1).
GN BFB1
OS Bos taurus (Bovine).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Bovidae; Bovinae; Bos.
CX NCBI TaxId:9913.
SQ SEQUENCE FROM N.A.
RX MEDLINE:9614778. PubMed:348394.
RA Tarter, A.P., Clark, D.P., Diamond, G., Russell, C.F.,
RA Erdjument-Bronage, H., Tempst, P., Cohen, K.S., Jones, O.E., Sweeney, R.W.,
RA Mines, M., Wang, S., Bevins, C.L.;
RT "Enteric beta-defensin: molecular cloning and characterization of a
RT gene with inducible intestinal, epithelial cell expression associated
RT with cryptosporidium parvum infection."
RL Infect. Immun. 66:1045-1056(1998).
EN
SQ SEQUENCE FROM N.A.
RX MEDLINE:9604277. PubMed:859522.
RA Gallagher, S.G., Ryan, A.M., Diamond, G., Bevins, C.L., Knoch, J.E.,
RT "Scallop coel mapping of beta-defensin genes to cattle syntenic group
RT U25 and fluorescence in situ localization to chromosome 27."
RL Mamm. Genome 6:554-556(1995).
CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY (POTENTIAL).
CC -1- TISSUE SPECIFICITY: INDUCIBLY EXPRESSED IN ENTERIC EPITHELIAL
CC CELLS.
CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP
CC SUBFAMILY.
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CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC EVL: A030022; AAC4805.1.
CC DR HSP: A03059.1; AAC4804.1.
CC DR HSP: P4670; IBB.
CC InterPro: IPR01855; Defensin_beta.
CC Plan: PF0771; Defensin_beta.1.
CC SMART: SM00048; DEFEN.1.
CC Anticibiotic_Signal.
CC PQ: A030022; AAC4805.1.
CC EVL: A03059.1; AAC4804.1.
CC DR HSP: P4670; IBB.
CC InterPro: IPR01855; Defensin_beta.
CC Plan: PF0771; Defensin_beta.1.
CC SMART: SM00048; DEFEN.1.
CC Anticibiotic_Signal.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 64 ENTERIC BETA-DEFENSIN.
FT DISULFID 38 50 BY SIMILARITY.
FT DISULFID 43 61 BY SIMILARITY.

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SQ SEQUENCE 64 AA: 7426 MW: 78642AB6F7A5668 CRC64.
Query Match 31.8% Score 78.5; DB 1; Length 64;
Best Local Similarity 42.1% Pred. No. 0 COL1;
Matches 18: Conservative 2; Mismatches 19; Indels 3; Gaps 0;

QY 1 GIMTQYVCPVRCRCVAVSLPKBEQIGKSTPRKCR 42
DB 24 GIMRPS---CPMNGICVPIPCPNLRQVGIPTPVACCR 62

RESULT 5
ID_BDI_DUG STANDARD PRT: 64 AA.
AC G45572.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-2001 (Rel. 42, Last annotation update)
DE Beta-defensin 1; Precursor (SD-1) (Defensin, beta 1).
GN BFB1
OS Bos taurus (Bos).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
CX NCBI TaxId:9913.
SQ SEQUENCE FROM N.A.
RX MEDLINE:9614778. PubMed:348394.
RA Tarter, A.P., Clark, D.P., Diamond, G., Russell, C.F.,
RA Erdjument-Bronage, H., Tempst, P., Cohen, K.S., Jones, O.E., Sweeney, R.W.,
RA Mines, M., Wang, S., Bevins, C.L.;
RT "Enteric beta-defensin: molecular cloning and characterization of a
RT gene with inducible intestinal, epithelial cell expression associated
RT with cryptosporidium parvum infection."
RL Infect. Immun. 66:1045-1056(1998).
EN
SQ SEQUENCE FROM N.A.
RX MEDLINE:9604277. PubMed:859522.
RA Gallagher, S.G., Ryan, A.M., Diamond, G., Bevins, C.L., Knoch, J.E.,
RT "Scallop coel mapping of beta-defensin genes to cattle syntenic group
RT U25 and fluorescence in situ localization to chromosome 27."
RL Mamm. Genome 6:554-556(1995).
CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY (POTENTIAL).
CC -1- TISSUE SPECIFICITY: INDUCIBLY EXPRESSED IN ENTERIC EPITHELIAL
CC CELLS.
CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC EVL: A030022; AAC4805.1.
CC DR HSP: A03059.1; AAC4804.1.
CC DR HSP: P4670; IBB.
CC InterPro: IPR01855; Defensin_beta.
CC Plan: PF0771; Defensin_beta.1.
CC SMART: SM00048; DEFEN.1.
CC Anticibiotic_Signal.
CC PQ: A030022; AAC4805.1.
CC EVL: A03059.1; AAC4804.1.
CC DR HSP: P4670; IBB.
CC InterPro: IPR01855; Defensin_beta.
CC Plan: PF0771; Defensin_beta.1.
CC SMART: SM00048; DEFEN.1.
CC Anticibiotic_Signal.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 64 ENTERIC BETA-DEFENSIN.
FT DISULFID 38 50 BY SIMILARITY.
FT DISULFID 43 61 BY SIMILARITY.

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[illegible]

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Best Local Similarity 36.18; PseudNo. 0.16;
Matches 13; Conservative 4; Mismatches 16; Gaps 2

QY 13 CVRGRGCAVLS-CFKEEIQKSTGK-KCSR 43
DB 26 CVRGRGCFPKKICIPESQFQNDCKWAKCKK 61
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RESULT 12
UP0216 PRELIMINARY: PRT: 67 AA.
AC C
CT C
DT 01-JUN-2003 (TREMUR): 21; Created
DT 01-JUN-2003 (TREMUR): 21; Last sequence update
DT 01-MAR-2003 (TREMUR): 21; Last annotation update
DE Phrative beta defensin.
GN DEF89.
GC
CC Mus musculus 'Mouse'
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eupleistonia;
CC Mammalia; Eumammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC 'M.'; TaxId=10109.
RN
PC STRAHC65B/6N; TSS=EBBrain;
PC Norrison G., Sewell C.G., Kilarski F., Hill R., Dorin J.
PC "Identification of murine beta defensin genes."
PC Submitted MAR-2-02 to the EMBL/GenBank/CCDB databases.
IR EMBL: AC11047; CAZ24896.1.
SC
SEQUENCE 67 AA; 3412 MW. 359;CACDCCSEIA74 CR554.
Query Match 25.43; Score 53.5; DB 11; Length 67;
Best Local Similarity 25.54; PseudNo. 0.16;
Matches 13; Conservative 6; Mismatches 24; Indels 1; Gaps 1

QY 2 INTLKYVVEGQAVLSCLEKFEQIKSTGKGRCKK 45
DB 25 IYVSEMPCHKGGYCVFICFSHKKIKGCFWPKRCKIK 67
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RESULT 13
UP0216 PRELIMINARY: PRT: 90 AA
AC C
CT C
DT 01-MAR-2003 (TREMUR): 15; Created
DT 01-MAR-2003 (TREMUR): 15; Last sequence update
DT 01-MAR-2003 (TREMUR): 21; Last annotation update
DE E2E2.
OS Homo sapiens 'Human'
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OS Mammalia; Eumammalia; Primates; Catarrhini; Hominiidae; Homo.
CC 'H.'; TaxId=9606.
RN
PC STRAHC65B/6N; TSS=EBBrain;
PC Frolisch O., PC C., Young L.G.;
PC "Genomic organization of the human epididymal E2f gene and its
PC relationship to defensin genes."
PC Submitted MAY-2-03 to the EMBL/GenBank/CCDB databases.
IR EMBL: AT053249; AAC22882.1.
SC
SEQUENCE 90 AA; 9391 MW. CF3DE9870584C19 CR646.
Query Match 25.24; Score 63; DB 4; Length 90;
Best Local Similarity 34.18; PseudNo. 0.22;
Matches 14; Conservative 7; Mismatches 16; Indels 4; Gaps 1

QY 1 GILNTLYKVRVEGRCVAVLSCLPKEEICKSTGRCKC 41
DB 24 GSRATL----CRVQGGICRLFFCHSGKRGKICSPQNRRC 60
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RESULT 14
UP0226 PRELIMINARY: PRT: 90 AA.
AC C
CT C
DT 01-JUN-2003 (TREMUR): 21; Created
DT 01-JUN-2003 (TREMUR): 21; Last sequence update
DT 01-MAR-2003 (TREMUR): 21; Last annotation update
DE Phrative beta defensin.
GN DEF89.
GC
CC Mus musculus 'Mouse'
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eupleistonia;
CC Mammalia; Eumammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC 'M.'; TaxId=10109.
RN
PC STRAHC65B/6N; TSS=EBBrain;
PC Norrison G., Sewell C.G., Kilarski F., Hill R., Dorin J.
PC "Identification of murine beta defensin genes."
PC Submitted MAR-2-02 to the EMBL/GenBank/CCDB databases.
IR EMBL: AC11047; CAZ24896.1.
SC
SEQUENCE 67 AA; 3412 MW. 359;CACDCCSEIA74 CR554.
Query Match 25.43; Score 53.5; DB 11; Length 67;
Best Local Similarity 25.54; PseudNo. 0.16;
Matches 13; Conservative 6; Mismatches 24; Indels 1; Gaps 1

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AC Q9M226;
DT 01-OCT-2000 (TrEMBLrel. 15, Created);
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 21, Last annotation update);
DE P2 protein variant E;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
RX 11_B_TaxID=9594;
RP SEQUENCE FROM N.A.
RS PSL:INS2027701; PubMed:10819450;
RA Frolich O., Po C., Murphy T., Young L.G.;
RT "Multiple promoter and splicing mRNA variants of the epididymis-
FT specific gene EP2.";
RL J. Androl. 21:421-436(2000);
DR EMBL: AF263555; AAF87722.1;
SQ SEQUENCE 90 AA; 9107 MW; CF21F5856C744019 CRC64;

Query Match: 25.28; Score 63; DB 5; Length 90;
Best Local Similarity: 34.11; Pct. Id. 6.22; 16; Indels 4; Gaps 1;
Matches 14; Conservative

CY 1 GIINTLQYKVRGRCAGVLSCLPKKEQIGKSTGRKCC 4;
DB 24 GIRNTI---CRMQGGCRJFFCHSGEKXKDCSDENHCC 63

RESULT 15
Q9M226 PRELIMINARY: PRT: 50 AA
AC Q9M226;
DT 01-MAR-2002 (TrEMBLrel. 20, Created);
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update);
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update);
DE Sperm protamine P1;
OS Nematoda; Euteleostomi;
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Chiroptera; Microchiroptera; Natulidae; Natalus.
RX 13_B_TaxID=155040;
RP SEQUENCE FROM N.A.
RS STRAIN=TK5660;
RA Van Den Bussche P.A., Hofer S.R., Hansen E.M.;
RT "Characterization and phylogenetic utility of the mammalian protamine
P1 gene.";
RL Mol. Phylogenet. Evol. 21:9-012001;
CC -!- FUNCTION: PROTIMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM NUCLEI INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PROTIMINE P1 FAMILY.
DR EMBL: AF435937; RAJ3571.1;
DE InterPro: IPR000221; Protamine P1;
DR Pfam: PF00250; Protamine P1; 1;
DR PROSITE: PS00048; PROTIMINE P1; 1;
KW Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
KW Nucleosome core; Spermatogenesis;
SQ SEQUENCE 50 AA; 6678 MW; 042E955A3A1C0E CRC64;

Query Match: 24.81; Score 62; DB 5; Length 50;
Best Local Similarity: 32.64; Pct. Id. 6.22; 10; Indels 12; Gaps 1;
Matches 14; Conservative

CY 6 LQNYKVRGRCAGVLS---CLPKKEGIGKSTGRKCC 45
DB 1 MARYRC -----CRGSRGRCRPRP---KSTPRACCRKP 14

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Search completed: October 27, 2003, 14:54:15
 Job time: 37 secs

GenScope version 5.1.4
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QM protein - protein search, using sw model

Run on: October 27, 2003, 14:52:02, Search time 16 Seconds
Without alignments, 118,999 Million cell updates/sec

Title: US-09-872-852-4
Prefix score: 70.5
Sequence: 1 GINTLQYVYVGRVGRVAVKREGICKSTPQKCRPKK 45

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 3287.7 seqs, 4210858 residues

Total number of hits satisfying chosen parameters: 32877

Minimum DB seq length: 9

Maximum DB seq length: 200506030

Post-processing: Minimum Match 01

Maximum Match 1031

Listing first 45 summaries

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2 /sgn2_6/prodata/2/aa/5B_COMB.pep.
3 /sgn2_6/prodata/2/aa/5C_COMB.pep.
4 /sgn2_6/prodata/2/aa/5D_COMB.pep.
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6 /sgn2_6/prodata/2/aa/5F_COMB.pep.
7 /sgn2_6/prodata/2/aa/5G_COMB.pep.
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45 /sgn2_6/prodata/2/aa/5AS_COMB.pep.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	250	100.0	45	4	US-09-868-659-2	Sequence 2, Appl
2	250	100.0	67	4	US-09-868-659-4	Sequence 4, Appl
3	250	100.0	67	4	US-09-868-659-10	Sequence 10, Appl
4	240	96.0	65	4	US-09-836-399A-2	Sequence 2, Appl
5	214	95.6	42	4	US-09-836-399A-21	Sequence 41, Appl
6	214	95.6	47	4	US-09-836-399A-15	Sequence 15, Appl
7	214	95.6	47	4	US-09-836-399A-17	Sequence 17, Appl
8	214	95.6	47	4	US-09-836-399A-19	Sequence 19, Appl
9	214	95.6	47	4	US-09-836-399A-15	Sequence 15, Appl
10	209	81.6	46	4	US-09-836-399A-44	Sequence 44, Appl
11	209	81.6	46	4	US-09-836-399A-42	Sequence 42, Appl
12	209	81.6	46	4	US-09-836-399A-43	Sequence 43, Appl
13	209	81.6	47	4	US-09-836-399A-39	Sequence 39, Appl
14	209	81.6	47	4	US-09-836-399A-35	Sequence 35, Appl
15	208	81.2	44	4	US-09-836-399A-2	Sequence 2, Appl
16	208	81.2	44	4	US-09-836-399A-2	Sequence 2, Appl
17	204	81.6	43	4	US-09-836-399A-47	Sequence 47, Appl
18	204	81.6	43	4	US-09-836-399A-21	Sequence 21, Appl
19	203	81.2	43	4	US-09-836-399A-46	Sequence 46, Appl
20	203	81.2	43	4	US-09-836-399A-46	Sequence 46, Appl
21	200	90.0	42	4	US-09-836-399A-49	Sequence 49, Appl
22	200	90.0	42	4	US-09-836-399A-49	Sequence 49, Appl
23	199	79.6	42	4	US-09-836-399A-46	Sequence 46, Appl
24	199	79.6	42	4	US-09-836-399A-46	Sequence 46, Appl
25	199	79.6	42	4	US-09-836-399A-46	Sequence 46, Appl
26	199	79.6	42	4	US-09-836-399A-46	Sequence 46, Appl
27	199	79.6	42	4	US-09-836-399A-46	Sequence 46, Appl

28	194	71.6	41	4	US-09-836-399A-25	Sequence 25, Appl
29	194	71.6	41	4	US-09-836-399A-25	Sequence 25, Appl
30	194	71.6	41	4	US-09-836-399A-25	Sequence 25, Appl
31	194	71.6	41	4	US-09-836-399A-25	Sequence 25, Appl
32	189	75.6	40	4	US-09-836-399A-28	Sequence 28, Appl
33	189	75.6	40	4	US-09-836-399A-32	Sequence 32, Appl
34	189	75.6	40	4	US-09-836-399A-32	Sequence 32, Appl
35	189	75.6	40	4	US-09-836-399A-52	Sequence 52, Appl
36	189	75.6	40	4	US-09-836-399A-52	Sequence 52, Appl
37	189	75.6	40	4	US-09-836-399A-52	Sequence 52, Appl
38	189	75.6	40	4	US-09-836-399A-52	Sequence 52, Appl
39	189	75.6	40	4	US-09-836-399A-52	Sequence 52, Appl
40	189	75.6	40	4	US-09-836-399A-52	Sequence 52, Appl
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42	189	75.6	40	4	US-09-836-399A-52	Sequence 52, Appl
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45	189	75.6	40	4	US-09-836-399A-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-09-868-659-2
Sequence 2, Application US/0948659
Parent No. 558002

GENERAL INFORMATION:

APPLICANT: CHRISTOPHERS, ERNO
APPLICANT: HARZER, JURGEN
APPLICANT: SCHROEDER, JENS
TITLE OF INVENTION: HUMAN ANTIBIOTIC PROTEINS
FILE REFERENCE: EP 187A
CURRENT APPLICATION NUMBER: US/09/868,659
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: PCT/EP03/05776
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: DE 199 05 128.9
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: DE 199 49 436.3
PRIOR FILING DATE: 1999-10-06
INVENTOR: SEO, ILKANG
SOFTWARE: SEQ ID NO. 8
PARENT: Patent No. 2.1
SEQ ID NO. 2
LENGTH: 45
TYPE: PRT
ORGANISM: Homo sapiens
US-09-868-659-2

Query Match: 100.0%, Score 250.0, DB 4, Length 45
Best Local Similarity: 100.0%, Fred No. 1.5e-24, Index 0
Mismatch: 45, Conservative: 0, Mismatch: 0

QY: 1 GINTLQYVYVGRVGRVAVSLPKEICKGKSTPQKCRPKK 45

CS: 1 GINTLQYVYVGRVGRVAVSLPKEICKGKSTPQKCRPKK 45

RESULT 2

US-09-868-659-4
Sequence 4, Application US/0948659
Parent No. 558002
GENERAL INFORMATION:
APPLICANT: CHRISTOPHERS, ERNO
APPLICANT: HARZER, JURGEN
APPLICANT: SCHROEDER, JENS
TITLE OF INVENTION: HUMAN ANTIBIOTIC PROTEINS
FILE REFERENCE: EP 187A
CURRENT APPLICATION NUMBER: US/09/868,659
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: PCT/EP03/05776
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: DE 199 05 128.9

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1 PRIOR FILING DATE: 1999-02-01
2 PRIOR APPLICATION NUMBER: 60/364,294
3 PRIOR FILING DATE: 1997-11-05
4 PRIOR APPLICATION NUMBER: 09/159,766
5 PRIOR FILING DATE: 1998-09-10
6 PRIOR APPLICATION NUMBER: 09/636,399
7 NUMBER OF SEQ ID NOS: 72
8 SOFTWARE: FASTSEQ for Windows Version 3.0
9 SEQ ID NO: 2
10 TYPE: PRT
11 ORGANISM: Homo sapiens
12 US-09-636-399A-2
13
14 Query Match
15 Best Local Similarity: 100.0%; Score 240; DB 4; Length 67;
16 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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18 QY 1 GIINTLQKYVVRGRCVAVLSCLPKEQIGKSTGRKCKRKK 45
19 DB 23 GIINTLQKYVVRGRCVAVLSCLPKEQIGKSTGRKCKRKK 67
20
21 RESULT 3
22 US-09-636-399A-10
23 Sequence 2, Application US/09636399A
24 Patent No. 6576755
25 GENERAL INFORMATION:
26 APPLICANT: Adler, David A.
27 APPLICANT: Holloway, James L.
28 APPLICANT: Bandaru, Nand
29 APPLICANT: Beigel-Orne, Stephanie
30 APPLICANT: Sheppard, Paul G.
31 TITLE OF INVENTION: NOVEL BETA-DEFENSINS
32 FILE REFERENCE: 97-4402
33 CURRENT APPLICATION NUMBER: US/09/636,399A
34 PRIOR APPLICATION NUMBER: 60/364,294
35 PRIOR FILING DATE: 1997-11-05
36 PRIOR APPLICATION NUMBER: 09/159,766
37 PRIOR FILING DATE: 1998-09-10
38 PRIOR APPLICATION NUMBER: 09/636,399
39 NUMBER OF SEQ ID NOS: 72
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41 TYPE: PRT
42 ORGANISM: Homo sapiens
43 US-09-636-399A-10
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52 RESULT 4
53 US-09-636-399A-2
54 Sequence 2, Application US/09636399A
55 Patent No. 6576755
56 GENERAL INFORMATION:
57 APPLICANT: Adler, David A.
58 APPLICANT: Holloway, James L.
59 APPLICANT: Bandaru, Nand
60 APPLICANT: Beigel-Orne, Stephanie
61 APPLICANT: Sheppard, Paul G.
62 TITLE OF INVENTION: NOVEL BETA-DEFENSINS
63 FILE REFERENCE: 97-4402
64 CURRENT APPLICATION NUMBER: US/09/636,399A
65 PRIOR FILING DATE: 2000-08-10
66 SEQ ID NO: 1
67 TYPE: PRT
68 ORGANISM: Homo sapiens
69 US-09-636-399A-10
70
71 Query Match
72 Best Local Similarity: 100.0%; Score 240; DB 4; Length 67;
73 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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75 QY 1 GIINTLQKYVVRGRCVAVLSCLPKEQIGKSTGRKCKRKK 45
76 DB 23 GIINTLQKYVVRGRCVAVLSCLPKEQIGKSTGRKCKRKK 67
77
78 RESULT 5
79 US-09-636-399A-43
80 Sequence 43, Application US/0636399A
81 Patent No. 6576755
82 GENERAL INFORMATION:
83 APPLICANT: Adler, David A.
84 APPLICANT: Holloway, James L.
85 APPLICANT: Bandaru, Nand
86 APPLICANT: Beigel-Orne, Stephanie
87 APPLICANT: Sheppard, Paul G.
88 TITLE OF INVENTION: NOVEL BETA-DEFENSINS
89 FILE REFERENCE: 97-4402
90 CURRENT APPLICATION NUMBER: US/09/636,399A
91 PRIOR FILING DATE: 2000-08-10
92 PRIOR APPLICATION NUMBER: 60/364,294
93 PRIOR FILING DATE: 1997-11-05
94 PRIOR APPLICATION NUMBER: 09/159,766
95 PRIOR FILING DATE: 1998-09-10
96 PRIOR APPLICATION NUMBER: 09/636,399
97 NUMBER OF SEQ ID NOS: 72
98 SOFTWARE: FASTSEQ for Windows Version 3.0
99 SEQ ID NO: 43
100 TYPE: PRT
101 ORGANISM: Artificial Sequence
102 FEATURE:
103 OTHER INFORMATION: Defensin polypeptide
104 LOCATION: 1-41
105 OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
106 US-09-636-399A-43
107
108 Query Match
109 Best Local Similarity: 85.61; Score 214; DB 4; Length 45;
110 Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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115 RESULT 6
116 US-09-636-399A-41
117 Sequence 41, Application US/09636399A
118 Patent No. 6576755
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: PRIOR APPLICATION NUMBER: 09/150,786
: PRICE FILING DATE: 1998-03-10
: PRIOR APPLICATION NUMBER: 06/736,339
: PRICE FILING DATE: 2000-08-10
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 35
: LENGTH: 43

```

LOCATION: (45, ..., 45)
OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-C9-616-199A-15

Query Match 55.6% Score 214 DE 4 Length 40
Best Local Similarity 91.1% Pred. Pos. 5e 20
Matches 4 Conservative 0 Nonconservative 4
100%

CY

1 G I N T Q K Y C R V G G R C A V L S P F X E Q I K C S T S R K C C P R K K 49
| | | | | | | | | | | | | | | | | |
bB

5 G : N I P O L Y C K R V G G R C A V L S P F X E Q I G N S T R K C C X E R K 49
| | | | | | | | | | | | | | | | | |

RESULT 10
US-09-636-399A-44
; Sequence 44, Application US09636199A
; Patent No. 656765
; GENERAL INFORMATION

```

Query Match:      81.61  Score 269.   DB 4:   Length 44
Best Local Similarity 90.94  Pval. 0.19e-10
Matches 46;  Conservative 0;  Mismatches 4;  Indels
0
QY      : GIINTLCKYVYVVRGPGAVV-SCLPKEQVGRKSTROCKKXK 44
          |||||
DB       : GIINTLCKYVYVVRGPGAVV-SCLPKEQVGRKSTROCKKXK 44
          |||||

```

```

OY      : GIINTLCKYCYCRVGRGRCVLSCLPKESQ:3KCS7RGRKCRK 44
DB      : GIINTLCKYCYCRVGRGRCVLSCLPKESQ:3KCS7RGRKCRK 44

```

RESULT: 11
US-39-636-399A-42
: Sequence 42. Application US'09636399A

PRINT NO. 551755
OPERATION:
APPLICANT: Adulajev, James
APPLICANT: Haddock, James
APPLICANT: Berglund, Nanci
APPLICANT: Boiger, Orme, Stephanie
APPLICANT: Sheppard, Paul O
TITLE OF INVENTION: NOVEL BET-DEFENSINS
FILE REFERENCE: 97-4423
CURRENT APPLICATION NUMBER: 1567-99-016 1999A

Query Match 65.6%, Score 209, DB 4, Length 45;
 Best Local Similarity 60.91, Pred. No 1.9c-19;
 Matches 40; Conservative 0; Mismatches 4; Indels

1 GINTLQKYYCRVGGRCAYLSCLPKKECIGKCSTRGRKCRPK 44
| | | | |
2 GINTLQKYYCRVGGRCAYLSCLPKKECIGKYSTRGRKCRPK 49
| | | | |

REBUZZI, JAMES
US 93-608-395A-45
Sequence 47 Applicant UNCLE SAM'S
CROSSING SYSTEMS, INC.
APPLICANT ANDREW DAVIS
APPLICANT HOLLOMAN, James L.
APPLICANT BARNER, Ward
APPLICANT BEIGEL-ORR, Stephanie
APPLICANT SHEPARD, Paul C.
TITLE OF INVENTION: NOVEL BETA-DENSINS
FILE REFERENCE: 93-4462

```

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Defense polypeptide
NAME/KEY: VARIANT
LOCATION: 143..143

```

```

FEATURE:
OTHER INFORMATION: Defensin polypeptide
NAME/KEY: VARIANT
LOCATION: 143-149

```

RESULT: 11
US-39-636-399A-42
: Sequence 42. Application US'09636399A

OTHER INFORMATION: Xaa is Lev, Ile, Phe, Val, or Met.

US-09-636-399A-40

Query Match 83.61: Score 209; DP 4; Length 46;
Best Local Similarity 90.91; Pred. No. 2a-19;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
CY 1 GINTQKYCVRGRCVAVSLCPKEECIGKSTGRKCKRK 44
DB 3 GINTQKYCVRGRCVAVSLCPKEECIGKSTGRKCKRK 46

RESULT 13

US-09-636-399A-38
Sequence 38; Application US/09636399A

Patent No. 6576755

GENERAL INFORMATION:

APPLICANT: Asiles, David A.

APPLICANT: Holloway, James L

APPLICANT: Beiguel-Orme, Stephanie

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: NOVEL BETA-DEFENSINS

FILE REFERENCE: 97-4402

CURRENT APPLICATION NUMBER: US/09/636,399A

PRIOR FILING DATE: 2000-08-10

PRIOR APPLICATION NUMBER: 60/658,135

PRIOR FILING DATE: 1997-10-09

PRIOR APPLICATION NUMBER: 60/764,294

PRIOR FILING DATE: 1997-11-05

PRIOR APPLICATION NUMBER: 09/150,786

PRIOR FILING DATE: 1998-09-10

PRIOR APPLICATION NUMBER: 09/150,786

PRIOR FILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSeq for Windows Version 1.6

SEQ ID NO 38

LENGTH: 47

TYPE: PPT

ORGANISM: Artificial Sequence

OTHER INFORMATION: Defensin polypeptide

NAME/KEY VARIANT

LOCATION: 144...144

OTHER INFORMATION: Xaa is Lev, Ile, Val, Phe, or Met.

US-09-636-399A-38

Query Match 81.61: Score 209; DP 4; Length 47;
Best Local Similarity 90.91; Pred. No. 2a-19;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
CY 1 GINTQKYCVRGRCVAVSLCPKEECIGKSTGRKCKRK 44
DB 4 GINTQKYCVRGRCVAVSLCPKEECIGKSTGRKCKRK 47

RESULT 14

US-09-636-399A-36

Sequence 36; Application US/09636399A

Patent No. 6576755

GENERAL INFORMATION:

APPLICANT: Asiles, David A.

APPLICANT: Holloway, James L

APPLICANT: Beiguel-Orme, Stephanie

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: NOVEL BETA-DEFENSINS

FILE REFERENCE: 97-4402

CURRENT APPLICATION NUMBER: US/09/636,399A

PRIOR FILING DATE: 2000-09-10

PRIOR APPLICATION NUMBER: 60/658,135

PRIOR FILING DATE: 1997-10-09

PRIOR APPLICATION NUMBER: 60/764,294

PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/616,199
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 1.6
SEQ ID NO 36
LENGTH: 48
TYPE: PPT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Defensin polypeptide
NAME/KEY VARIANT
LOCATION: 145...145
OTHER INFORMATION: Xaa is Lev, Ile, Val, Phe, or Met.

US-09-636-399A-36

Query Match 93.61: Score 209; DP 4; Length 48;
Best Local Similarity 90.91; Pred. No. 2.1e-19;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
CY 1 GINTQKYCVRGRCVAVSLCPKEECIGKSTGRKCKRK 44
DB 5 GINTQKYCVRGRCVAVSLCPKEECIGKSTGRKCKRK 48

RESULT 15

US-09-636-399A-20

Sequence 20; Application US/09636399A

Patent No. 6576755

GENERAL INFORMATION:

APPLICANT: Asiles, David A.

APPLICANT: Holloway, James L

APPLICANT: Beiguel-Orme, Stephanie

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: NOVEL BETA-DEFENSINS

FILE REFERENCE: 97-4402

CURRENT APPLICATION NUMBER: US/09/636,399A

PRIOR FILING DATE: 2000-09-10

PRIOR APPLICATION NUMBER: 60/658,135

PRIOR FILING DATE: 1998-10-09

PRIOR APPLICATION NUMBER: 60/664,294

PRIOR FILING DATE: 1997-11-05

PRIOR APPLICATION NUMBER: 09/150,786

PRIOR FILING DATE: 1998-09-10

PRIOR APPLICATION NUMBER: 09/616,199

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSeq for Windows Version 1.6

SEQ ID NO 20

LENGTH: 48

TYPE: PPT

ORGANISM: Artificial Sequence

OTHER INFORMATION: Defensin polypeptide

US-09-636-399A-20

Query Match 81.61: Score 209; DP 4; Length 48;
Best Local Similarity 90.91; Pred. No. 2.5e-19;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
CY 2 LINTQKYCVRGRCVAVSLCPKEECIGKSTGRKCKRK 45
DB 1 LINTQKYCVRGRCVAVSLCPKEECIGKSTGRKCKRK 44

Search completed: October 27, 2003, 14:53:51
Cdb time: 16 secs

PT infections, particularly when incorporated in wound dressings, also
PT related nucleic acid
XX
PS Claim 1, Page 17, 41pp: German.
XX This invention describes the novel active, mature human proteins (1)
CC SAP-2 and SAP-3 which have antibiotic, antibacterial, antifungal and
CC antiviral activity, (2), and their precursors, are useful for treating
CC or preventing microbial infections caused by bacteria, fungi or
CC viruses, particularly where they for human cells expressing them, or
CC the human wound dressings and to produce specific antibodies or
CC antibodies against the dressings and against the variant, this sequence
CC deficiency of (1) or the presence of (2) variant, this sequence
CC represents the mature human SAP-3 protein described in the method of the
CC invention.
XX
XX
SQ Sequence 45 AA:
Query Match 100.0% Score 250; DB 23; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY : GINTLVKYYVWGRGCAVLSCLPKEQIKGKSTGRKCKRKK 45
DB : GINTLVKYYVWGRGCAVLSCLPKEQIKGKSTGRKCKRKK 45
AA017767
ID AA017767 standard; peptide; 45 AA.
XX
XX
AC AA017767;
XX
XX 30-AUG-2002 (first entry)
XX
XX Human beta-defensin-3 derivative #2.
XX
XX Human; beta-defensin-3; HBD-3; bacterial infection; gene therapy;
XX respiratory system; cystic fibrosis; inflammation; urogenital tract;
XX antibacterial; fungicide; cytostatic; antiinflammatory; antitumor;
XX Gastrointestinal tract; lepticemia; apoptosis induction; cancer.
XX
XX Homo sapiens.
XX
XX WC02024512 A2.
XX
XX 23-MAY-2002.
XX
XX 14-NOV-2001; 2001MO-EP13174.
XX
XX 14-NOV-2001; 2000DE-1056365
XX 30-MAR-2001; 2001DE-1016220.
XX
XX (EPP-1) 2PF PHARM GMEH.
XX
XX Bossmann W, Kluever B, Conejo Garcia J, Aderrmann K, Bais P,
XX Meegerik H,
XX
XX WFI; 2002-415956/46.
XX
XX New human beta-defensin 3, useful for treating or preventing microbial
XX infection and tumors, also related nucleic acid
XX
XX Claim 2, Page 23, 36pp: German.
XX
XX The present invention relates to human beta-defensin-3 (HBD-3) and its
XX derivatives. The peptides coding sequence, gene therapy and diagnostic
XX coding sequence are useful in gene therapy and diagnosis, especially
XX for preventing or treating a wide range of microbial infections
XX (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the
XX respiratory tract, especially in cases of cystic fibrosis), and
XX Helicobacter pylori, also inflammatory diseases of the gastrointestinal
XX and urogenital tracts, sepsis and yeast infections), and for inducing

CC apoptosis for treating malignant melanoma and tumors. The present
CC sequence is a derivative of human EB-3.
XX
XX Sequence 45 AA:
Query Match 100.0% Score 250; DB 23; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY : GINTLVKYYVWGRGCAVLSCLPKEQIKGKSTGRKCKRKK 45
DB : GINTLVKYYVWGRGCAVLSCLPKEQIKGKSTGRKCKRKK 45
AA097096
ID AA097096 standard; protein; 45 AA.
XX
XX AA097096;
XX
XX 24-MAR-2002 (first entry)
XX
XX Human beta-defensin-3 (HBD-3); mature protein sequence #2.
XX Human; antibacterial peptide; human beta-defensin-3; HBD-3;
XX microbial growth; microbial infection; pulmonary infection.
XX
XX Homo sapiens.
XX
XX WC02024512 A2
XX
XX 04-JFC 2001.
XX
XX 01-JUN-2001; 2001MO-2515057.
XX
XX 01-JUN-2001; 2000US-206792P.
XX
XX 110MA; UNIV IOWA RES FOUND.
XX
XX MSCRay PB, Task B, G.A HP, Schutte BC;
XX
XX WFI; 2002-156102/14.
XX
XX New human beta-defensin 3 peptides and nucleic acids encoding peptides,
XX useful for treating or preventing microbial growth or infection, or in
XX gene therapy
XX
XX Claim 2; Page 93; 110pp: English.
XX
XX The present invention relates to the isolation of a novel antimicrobial
XX peptide, human beta-defensin-3 (HBD-3). Also described is a method of
XX inhibiting growth of a microbe by introducing into a host or environment
XX the antimicrobial peptide of the invention. The peptide is useful for
XX treating or preventing microbial growth or infections, e.g. pulmonary
XX infections when administered by inhalation. The peptide can be applied
XX on a work surface or a surgical instrument for the prevention and/or
XX suppression of microbial growth. The present sequence represents
XX HBD-3 mature protein sequence #2.
XX
XX Sequence 45 AA.
Query Match 100.0% Score 250; DB 23; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY : GINTLVKYYVWGRGCAVLSCLPKEQIKGKSTGRKCKRKK 45
DB : GINTLVKYYVWGRGCAVLSCLPKEQIKGKSTGRKCKRKK 45
AA097094
ID AA097094 standard; protein; 45 AA.

[illegible]

XX Foremann K, Kluver E, Conde-Garcia J, Aderran K, Salis R
 PI Magill H
 XX WPI: 2002-415949/46
 XX New human beta-defensin 3, useful for treating or preventing microbial
 PT infection and tumors, also related nucleic acid
 XX Claim 2, Page 23, 16pp: German.
 XX The present invention relates to human beta-defensin 3 (hBD-3) and its
 CC derivatives. The peptide, its coding sequence and vectors containing the
 CC coding sequence are useful in gene therapy and diagnosis, especially
 CC for preventing or treating a wide range of microbial infections
 CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the
 CC respiratory tract, especially in cases of cystic fibrosis, and
 CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal
 CC and urogenital tracts, sepsis and yeast infections), and for inducing
 CC apoptosis for treating malignant melanoma and tumors. The present
 CC sequence is a derivative of human BD-3.
 XX Sequence 67 AA:
 Query Match 100.0%, Score 250, DP 23, Length 67
 Best Local Similarity 100.0%, Pred. No. 24-23;
 Matches 45, Conservative 0, Mismatches 0, Indels 0, Gaps 0
 QY 1 GINTLQKVCYRGRGVAVSLCLPKEGQVGTGRKCRKK 45
 DQ 23 GINTLQKVCYRGRGVAVSLCLPKEGQVGTGRKCRKK 67
 RESULT 7
 ID AAU51016
 AC AAU51016 standard: Peptide, 67 AA
 XX 05-JUN-2002 (first entry)
 XX Transplant media associated defensin peptide #17.
 XX Transplant, antimicrobial peptide, pore forming agent;
 KW cell surface receptor binding compound; kidney transplant;
 KW cardioplegia; organ transplant; transplant rejection; defensin.
 OS Homo sapiens.
 XX W0200209718-A1.
 XX 07-FEB-2002
 XX 27-JUL-2001: 2001WO-US21785.
 XX 28-JUL-2000: 2000US-221632P.
 XX 17-NOV-2000: 2000US-249602P.
 XX 15-MAY-2001: 2001US-290932P.
 XX MURPHY C J.
 PA MURPHY C J.
 PI Murphy C J., Reid TW, Mearns JF.
 XX WPI: 2002-268955/11.
 XX Media comprising antimicrobial polypeptides or pore forming agents
 PT and/or cell surface receptor binding compounds useful for the storage
 PT and preservation of organs prior to transplant.
 XX Claim 8, Page 29, 78pp: English
 XX The invention describes new transplant compositions comprising
 CC antimicrobial polypeptides or pore forming agents and/or cell surface
 CC receptor binding compounds. The media is capable of extending the
 CC preservation period past 72 hours and can provide organs with increased
 CC functionality upon transplant. Animals receiving kidneys stored in the
 CC media of the present invention for either three or four days had serum
 CC creatinine levels of less than half of those observed in control animals
 CC receiving kidneys stored in UW solution defined in the specification.

CC receptor binding compounds. The media is capable of extending the
 CC preservation period past 72 hours and can provide organs with increased
 CC functionality upon transplant. Animals receiving kidneys stored in the
 CC media of the present invention for either three or four days had serum
 CC creatinine levels of less than half of those observed in control animals
 CC receiving kidneys stored in UW solution defined in the specification.
 CC alone, lower serum creatinine levels are indicative of healthier kidneys
 CC and a more preferable prognosis for the transplant patient. The media of
 CC the invention are useful for decreasing the incidence and/or severity of
 CC delayed graft function in patients receiving transplanted kidneys stored
 CC and/or treated in the media. The media may also be used in procedures
 CC involving the preservation of organs. The media may also be used in
 CC an animal model to decrease transplant rejection. This sequence represents
 XX transplant media
 XX Sequence 67 AA:
 Query Match 100.0%, Score 250, DP 23, Length 67
 Best Local Similarity 100.0%, Pred. No. 24-23;
 Matches 45, Conservative 0, Mismatches 0, Indels 0, Gaps 0
 QY 1 GINTLQKVCYRGRGVAVSLCLPKEGQVGTGRKCRKK 45
 DQ 23 GINTLQKVCYRGRGVAVSLCLPKEGQVGTGRKCRKK 67
 RESULT 1
 ID AAU51016
 AC AAU51016 standard: Peptide, 67 AA
 XX 05-JUN-2002 (first entry)
 XX Transplant media associated defensin peptide #17.
 XX Transplant, antimicrobial peptide, pore forming agent;
 KW cell surface receptor binding compound; kidney transplant;
 KW cardioplegia; organ transplant; transplant rejection; defensin.
 OS Homo sapiens.
 XX W0200209718-A1.
 XX 07-FEB-2002
 XX 27-JUL-2001: 2001WO-US21785.
 XX 28-JUL-2000: 2000US-221632P.
 XX 17-NOV-2000: 2000US-249602P.
 XX 15-MAY-2001: 2001US-290932P.
 XX MURPHY C J.
 PA MURPHY C J.
 PI Murphy C J., Reid TW, Mearns JF.
 XX WPI: 2002-268955/31.
 XX Media comprising antimicrobial polypeptides or pore forming agents
 PT and/or cell surface receptor binding compounds useful for the storage
 PT and preservation of organs prior to transplant.
 XX Claim 8, Page 30, 78pp: English.
 XX The invention describes new transplant compositions comprising
 CC antimicrobial polypeptides or pore forming agents and/or cell surface
 CC receptor binding compounds. The media is capable of extending the
 CC preservation period past 72 hours and can provide organs with increased
 CC functionality upon transplant. Animals receiving kidneys stored in the
 CC media of the present invention for either three or four days had serum
 CC creatinine levels of less than half of those observed in control animals
 CC receiving kidneys stored in UW solution defined in the specification.

CC alone. Lower serum creatinine levels are indicative of healthier kidneys
 CC and a more preferable prognosis for the transplant patient. The media of
 CC the invention are useful for decreasing the incidence and/or severity of
 CC delayed graft function in patients receiving transplanted kidneys stored
 CC and/or treated in the media. The media may also be used in procedures
 CC such as catheterization, in conjunction with a transplant of healthier
 CC kidneys. The media of the invention are also useful for decreasing
 CC an antimicrobial defensin peptide included in the development of the
 CC transplant media.

XX Sequence 67 AA:

Query Match: 100.0%, Score 150, DB 23, Length 67.
 Best Local Similarity: 100.0%, Pred. No. 26-23.
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 GINTLQYGVVGGRCVAVGSCLPKKEETKCKSTRGRKCKPR 45
 DB 23 GINTLQYGVVGGRCVAVGSCLPKKEETKCKSTRGRKCKPR 67

RESULT 9

AAU09707

AAU09707 standard, Protein: 67 AA.

XX AC

XX AC

XX AC

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CC The present invention relates to the isolation of a novel antimicrobial
 CC peptide, human beta-defensin-3 (HBD-3). Also described is a method of
 CC inhibiting growth of a microbe by introducing into a host or environment
 CC the antimicrobial peptide of the invention. The peptide is useful for
 CC infections when administered by inhalation. The peptide can be applied
 CC on a work surface or a surgical instrument for the prevention and/or
 CC suppression of microbial growth. The present sequence represents
 CC HBD-3.

XX Sequence 67 AA:

Query Match: 100.0%, Score 150, DB 23, Length 67.
 Best Local Similarity: 100.0%, Pred. No. 26-23.
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 GINTLQYGVVGGRCVAVGSCLPKKEETKCKSTRGRKCKPR 45
 DB 23 GINTLQYGVVGGRCVAVGSCLPKKEETKCKSTRGRKCKPR 67

QY 1 GINTLQYGVVGGRCVAVGSCLPKKEETKCKSTRGRKCKPR 45
 DB 23 GINTLQYGVVGGRCVAVGSCLPKKEETKCKSTRGRKCKPR 67

RESULT 9

AAU09707

AAU09707 standard, Protein: 67 AA.

XX AC

XX AC

XX AC

XX AC

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CC This sequence represents the human zamp1 protein which is a member of the
 CC beta-defensin protein family. Zamp1 protein is useful as a pharmaceutical
 CC composition, useful for treatment of e.g. bacterial, fungal and viral
 CC infections. They are also useful pro-inflammatory, for treating chronic
 CC tissue damage, and for stimulating the immune response, for treatment of
 CC AIDS or chemotherapy patients. Zamp1 polypeptides and antibodies are
 CC useful for studying cellular and molecular biology, studying
 CC cell-cell interactions, and studying cyclooxygenase activity. Zamp1
 CC cells in culture, by incubation with the cells. Zamp1 polypeptides are
 CC especially useful for studying epithelial defensin induction in cell
 CC culture when exposed to pathogenic stimuli.

XX Sequence 65 AA:

Query Match: 96.0%, Score 240, DB 20, Length 65.
 Best Local Similarity: 100.0%, Pred. No. 336-22.
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 GINTLQYGVVGGRCVAVGSCLPKKEETKCKSTRGRKCKPR 43
 DB 23 GINTLQYGVVGGRCVAVGSCLPKKEETKCKSTRGRKCKPR 65

RESULT 11

AAU09708

AAU09708 standard, Protein: 65 AA.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

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XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

Adler C, Reinherz N, Belgut S, Holloway JL.

WP: 1999-215364/15.

N PSDB; AAX25985.

New zamp1 polypeptide and polynucleotide, human beta-defensins
 useful as diagnostic reagents and for treatment of microbial
 infections, and AIDS

Claim 1: Page 70, 79pp; English.

[illegible]

CC marker of inflammatory disease in epithelial organs. Both chronic and
CC acute diseases may be treated by localised gene therapy of the
CC encode regions can be used for systemic or localised gene
CC specified diseases in epithelial tissues or organs. (i) have exceptional
CC biological activity and since they do not induce an immune response, they
CC are particularly well suited for long-term use. This sequence represents
CC a human defensin described in the disclosure of the invention
XX
SQ Sequence 31 AA:
Query Match 70.8% Score 177 DB 23 Length 31:
Best Local Similarity 100.0% Pos. 98-15: C: indels C: Gaps D:
Matches 31: Conservative 0: Mismatches 0: indels C: Gaps D:
CY 11 CAVRGRCFVLSCLPKKEQIGKSTRGRKC 41
DB 1 CAVRGRCFVLSCLPKKEQIGKSTRGRKC 31
Search completed: October 27, 2003, 14:53:06
Job time : 43 secs